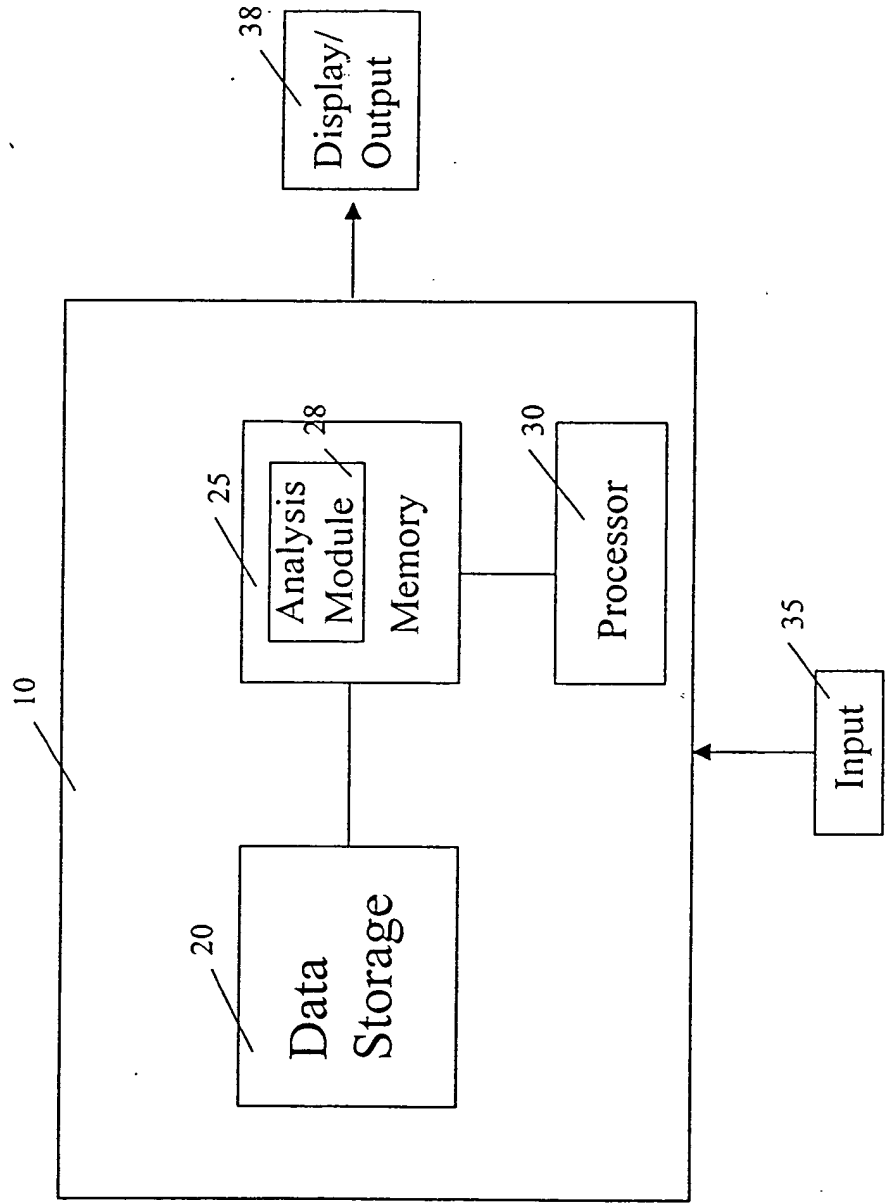


Figure 1

Figure 2



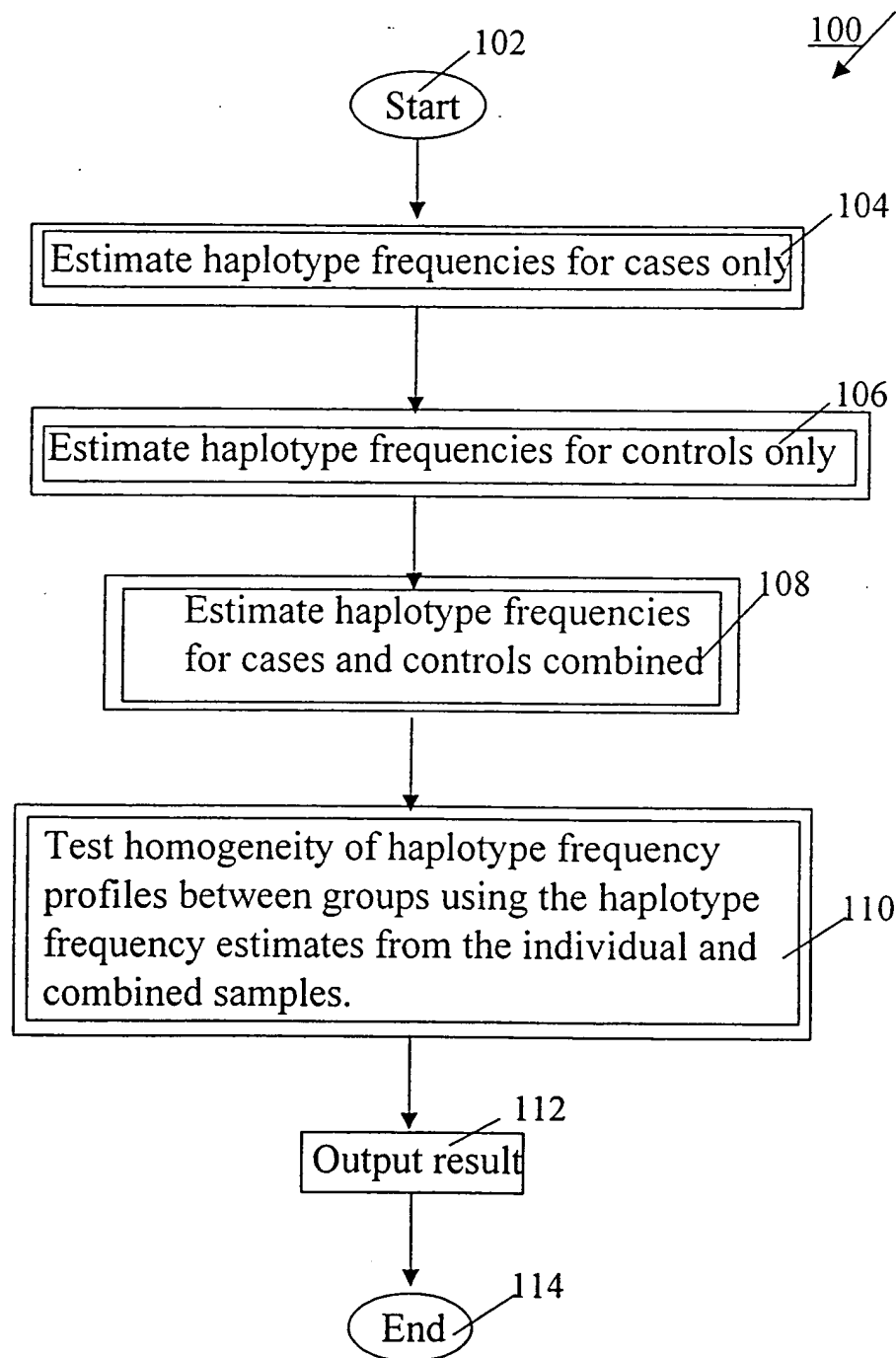


Figure 3

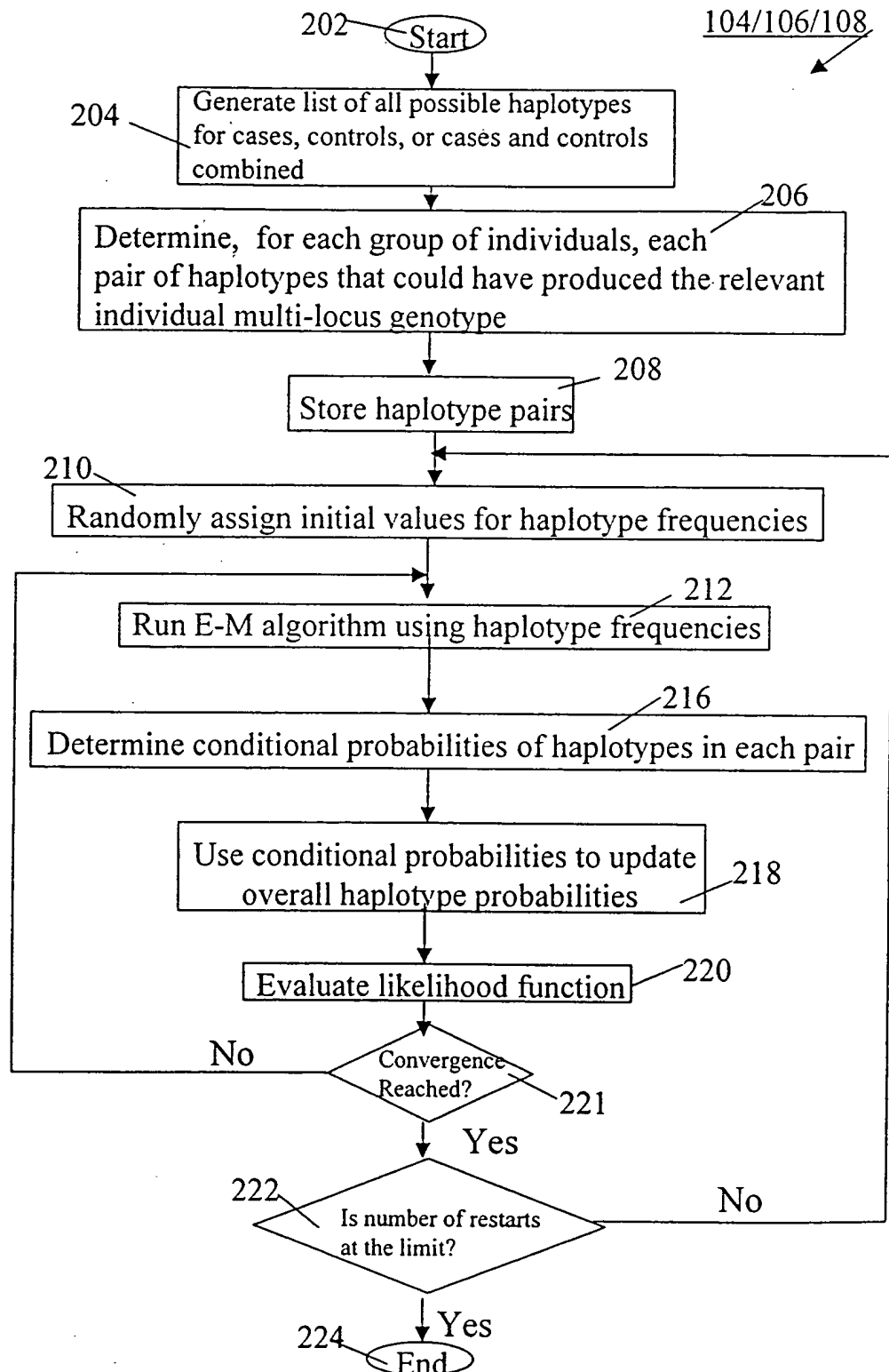


Figure 4

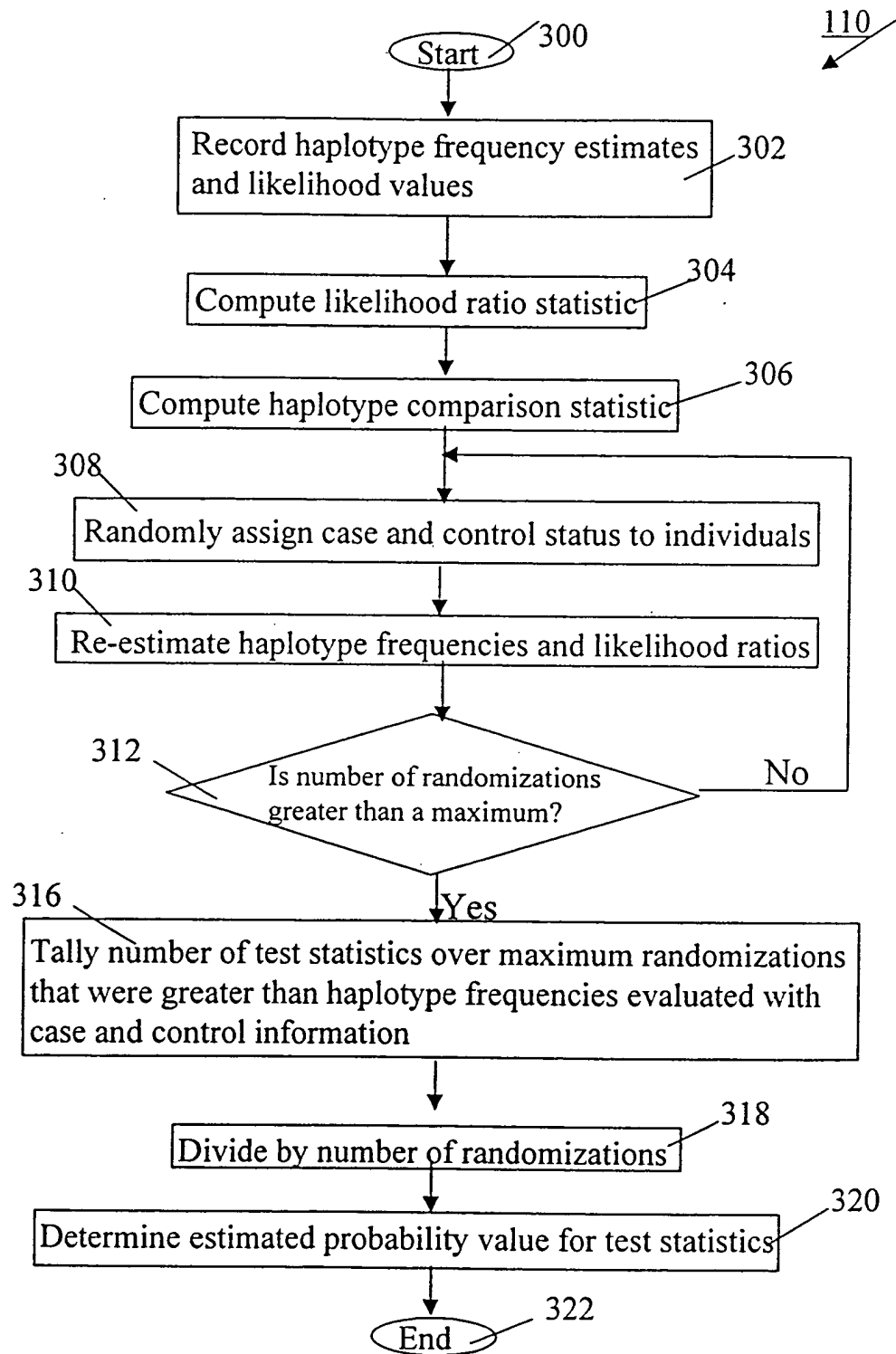


Figure 5

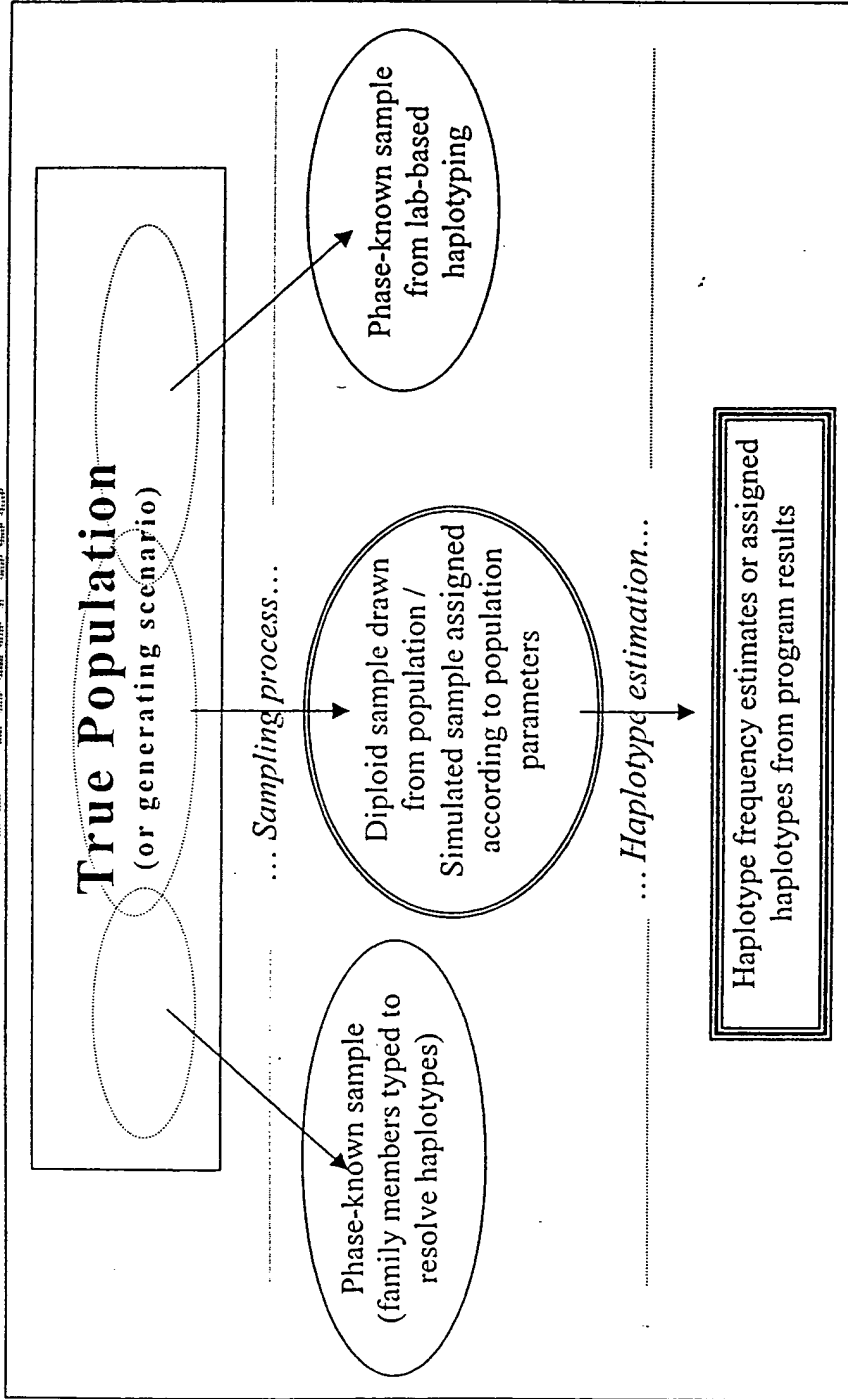


Figure 6

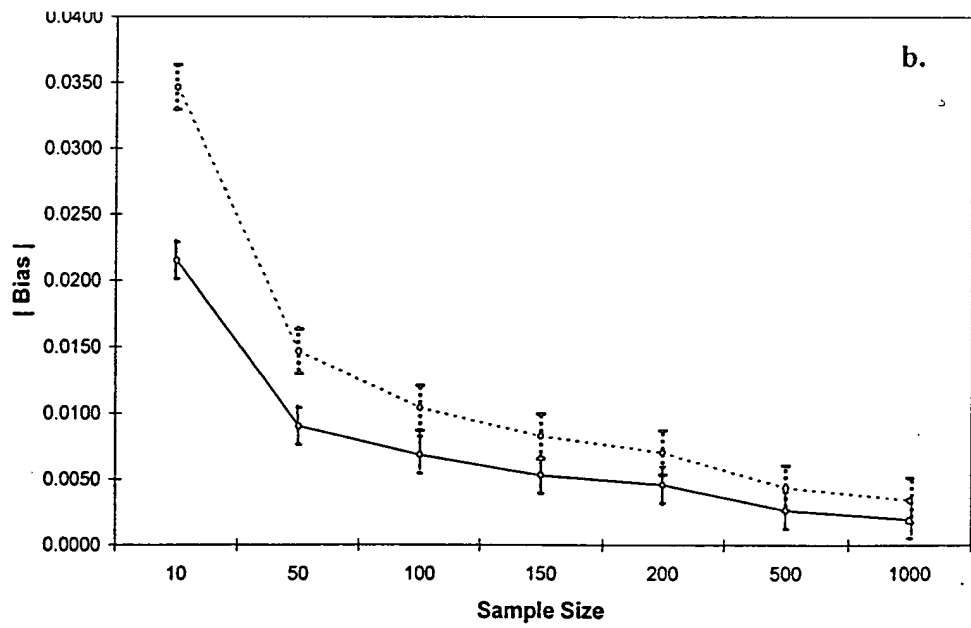
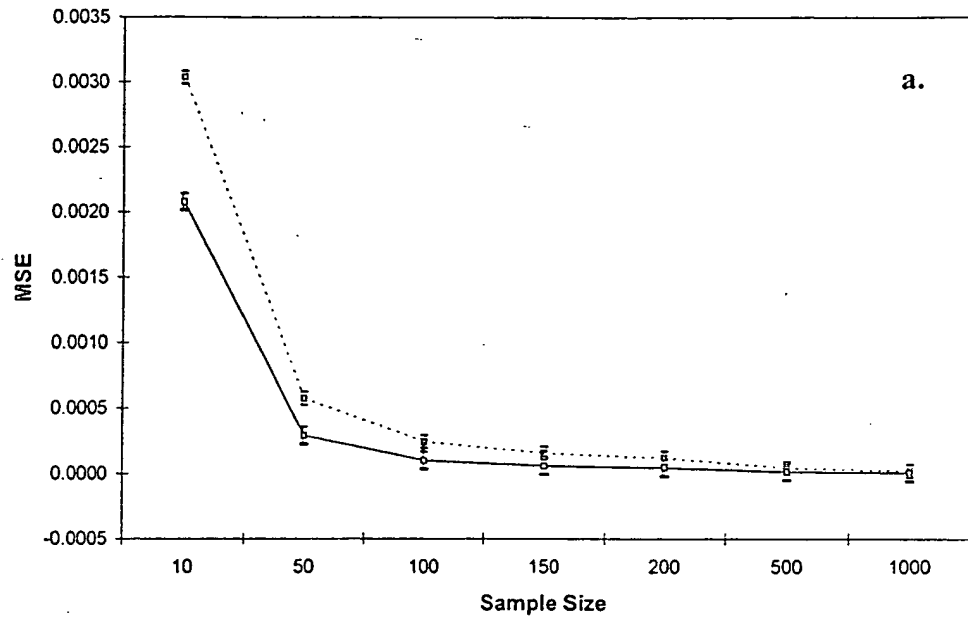


Figure 8

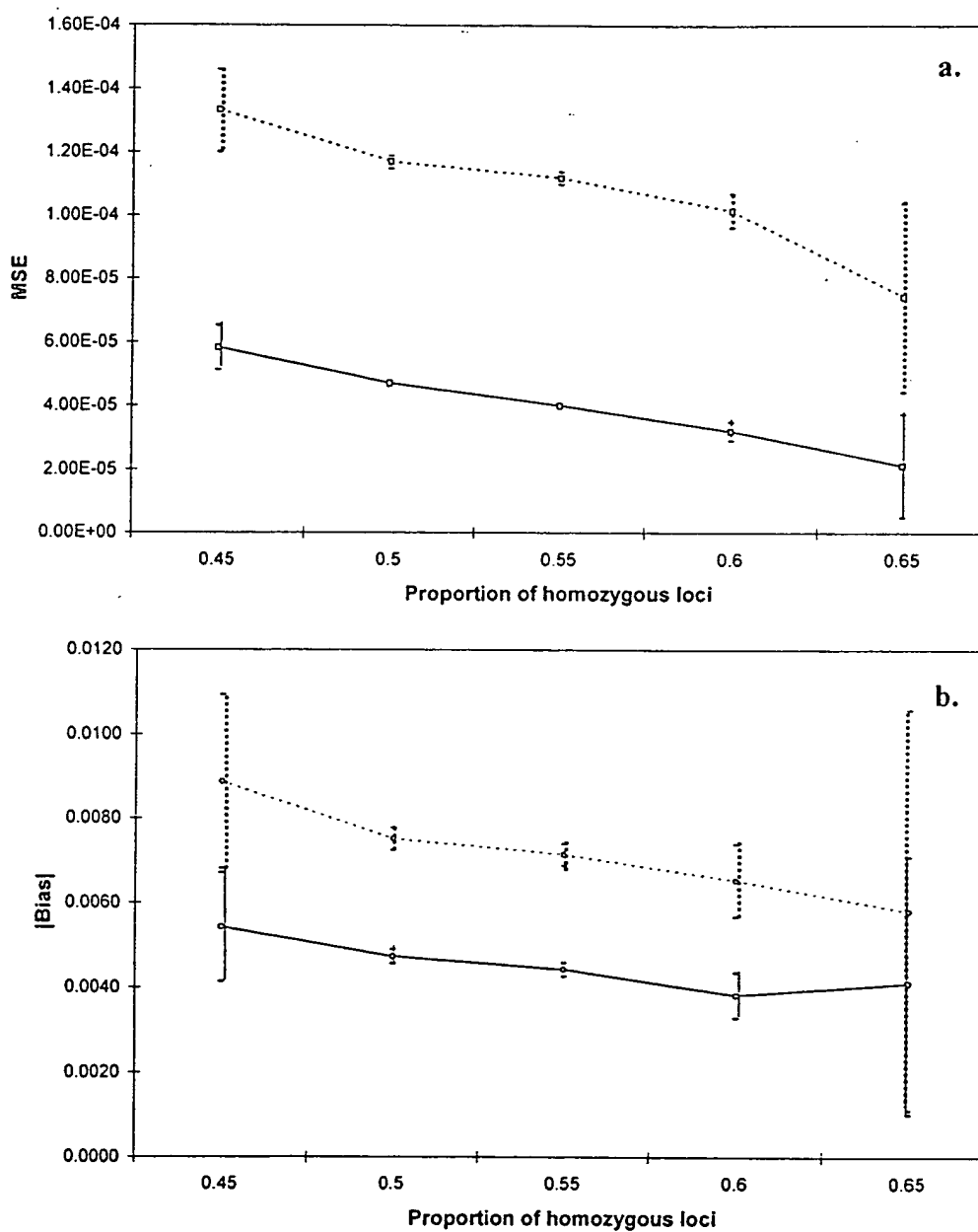


Figure 9

FO92E0-0928T860

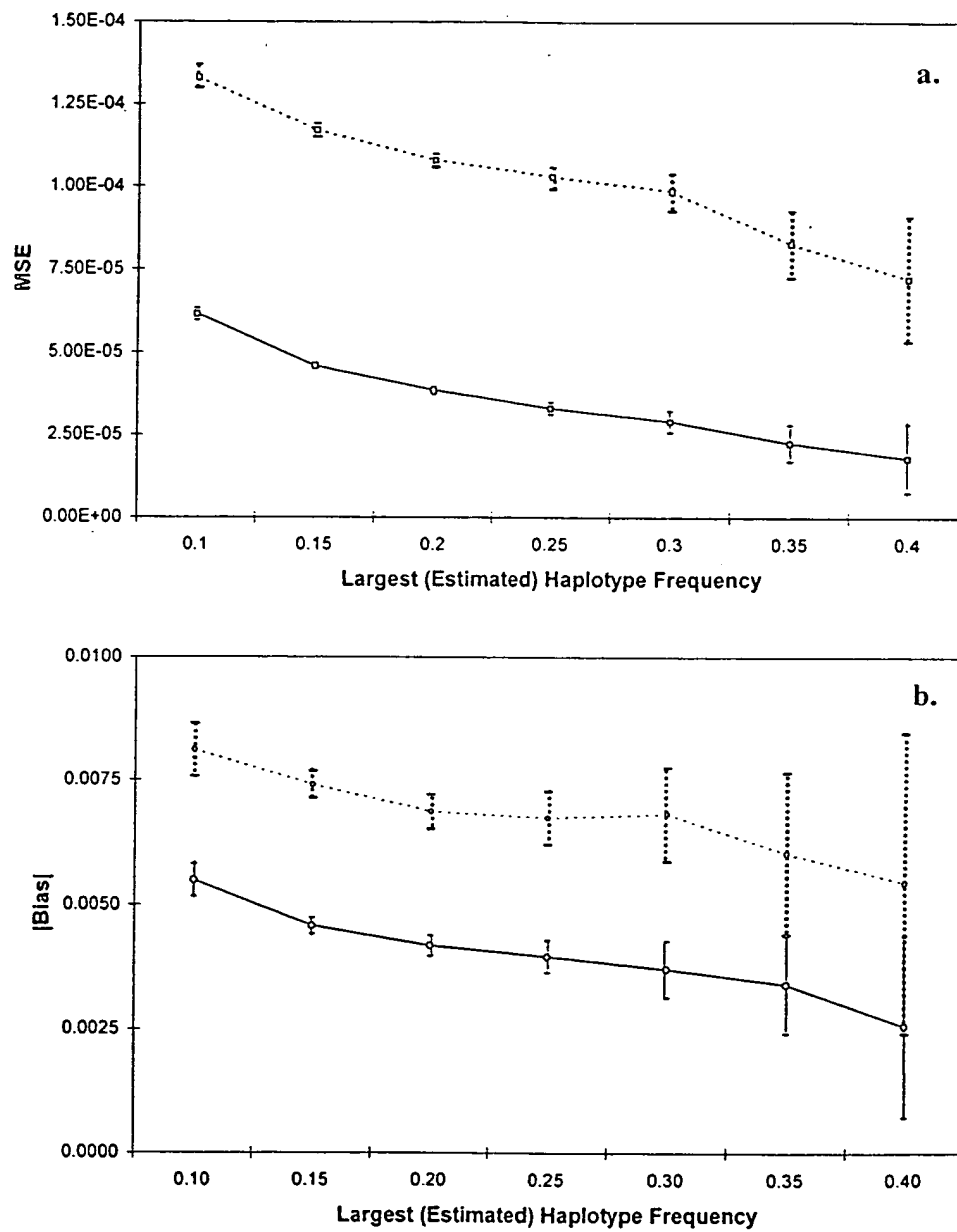


Figure 10

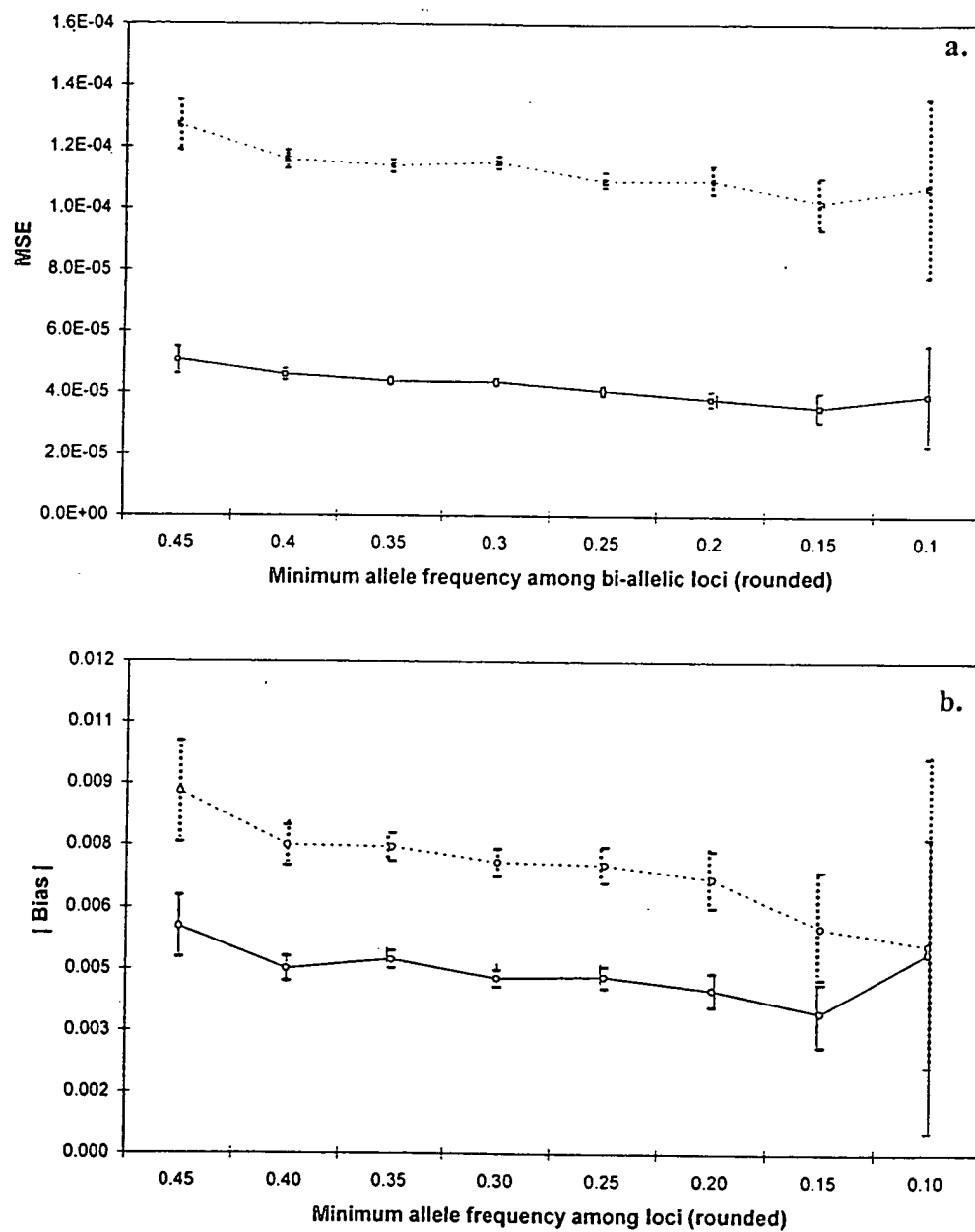


Figure 11

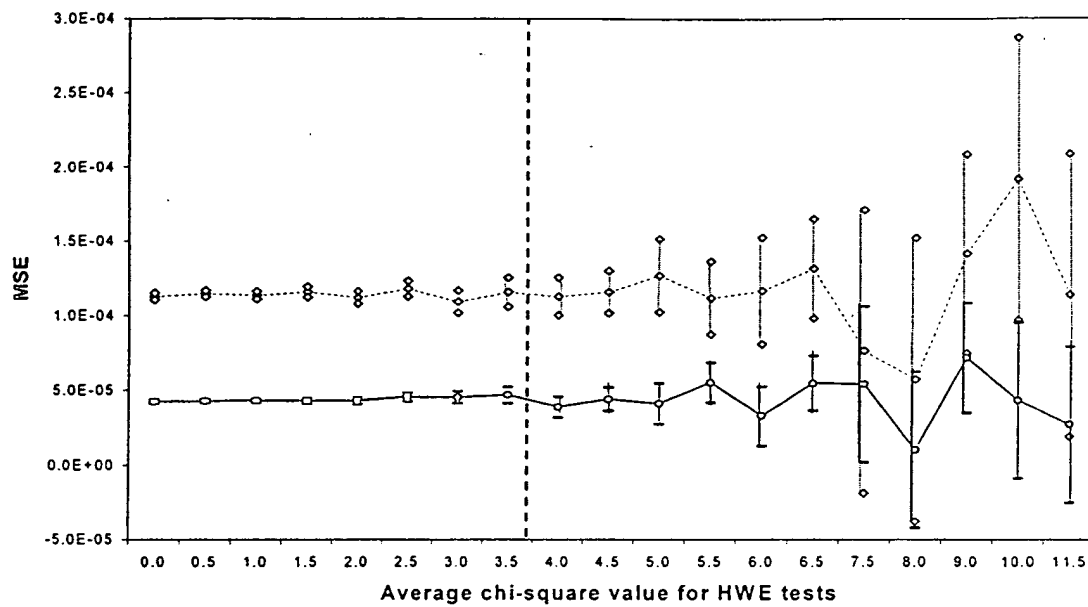


Figure 12

Table. Regression of absolute value of bias between estimated and generating haplotype frequencies on all factors.

Regression including all factors				Single-factor models		
Variable	Estimate	Std. Error	T test	Prob > T	R ²	F
2-locus Haplotypes:						
INTERCEP	0.031017	0.00220248	14.083	0.0001	0.0383	395.1818
Prop HOMOZ	-0.029256	0.00369778	-7.912	0.0001	0.0468	487.0159
Freq largest Hap.	-0.00238	0.00258249	-0.922	0.3568	0.0085	84.85
Chi-sq for LD	-3.0429E-05	0.00000383	-7.944	0.0001	0.0004	4.0044
H-W status	-0.000878	0.00080228	-1.094	0.274	0.0337	345.6019
Avg. Min Allele freq.	0.008471	0.00478999	1.769	0.077		
5-locus haplotypes:						
INTERCEP	0.058585	0.00499106	11.738	0.0001	0.0027	9.7079
PropHOMOZ	-0.004128	0.0033604	-1.229	0.2193	0.0085	30.2177
Freq largest Hap.	-0.007354	0.00163342	-4.502	0.0001	0.0452	166.6065
Avg D' for pairwise LD matrix	0.013172	0.00102619	12.836	0.0001	0.0002	0.8555
H-W status	-0.00155	0.00139011	-1.115	0.265	0.0001	0.3553
Avg. Min Allele freq.	-8.5172E-05	0.00038764	-0.22	0.8261		

Figure 14

Haplotype Estimation Results:

Hap No.	Haplotype	MLOCUS CEPHGP	SCHORK CEPHGP	PEDIGREE CEPHGP	MLOCUS BRCAtotal	SCHORK BRCAtotal	MLOCUS BRCAcase	SCHORK BRCAcase	MLOCUS BRCAcon	SCHORK BRCAcon
1	11111111	0.29210	0.29208	0.28280	0.21030	0.21687	0.23710	0.24214	0.20470	0.20564
2	11222111	0.20090	0.20085	0.20200	0.02750	0.01921	0.02510	0.02215	0.02700	0.01695
3	12222111	0.17790	0.17793	0.17680	0.14840	0.14497	0.21270	0.20714	0.10000	0.10101
4	12121111	0.11110	0.11111	0.10610	0.21090	0.21302	0.20120	0.18571	0.21360	0.22727
5	21111211	0.09290	0.09293	0.10100	0.16570	0.16256	0.15240	0.16429	0.16630	0.15626
6	11111112	0.08590	0.08586	0.09090	0.01560	0.01479	0.00000	0.00000	0.01820	0.02020
7	12111111	0.01400	0.01399	0.01520	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
8	11111121	0.02220	0.02222	0.02520	0.00560	0.00636	0.00000	0.00000	0.01000	0.01123
9	21111221	0.00300	0.00303	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
10	11221111	0.00000	0.00000	0.00000	0.18230	0.19231	0.14630	0.15714	0.20910	0.22042
11	11111211	0.00000	0.00000	0.00000	0.01870	0.01686	0.00000	0.00000	0.02630	0.02344
12	21111111	0.00000	0.00000	0.00000	0.00610	0.00608	0.00000	0.00000	0.01120	0.01041
13	21111212	0.00000	0.00000	0.00000	0.00000	0.00000	0.01220	0.00714	0.00000	0.00000
14	12111211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00680	0.00786	0.00000	0.00000
15	12222211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00610	0.00642	0.00000	0.00000
16	11222211	0.00000	0.00000	0.00000	0.00120	0.00150	0.00000	0.00000	0.00480	0.00000
17	11111221	0.00000	0.00000	0.00000	0.00250	0.00252	0.00000	0.00000	0.00420	0.00392
18	21121111	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00330	0.00000
19	21121211	0.00000	0.00000	0.00000	0.00260	0.00000	0.00000	0.00000	0.00130	0.00000
20	11221211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
21	12121112	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
22	11212121	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
23	21112211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000
24	12212211	0.00000	0.00000	0.00000	0.00260	0.00296	0.00000	0.00000	0.00000	0.00000
25	11112211	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00325
		1.00000	1.00000	1.00000	1.00000	1.00001	0.99990	0.99999	1.00000	1.00000

Figure 17

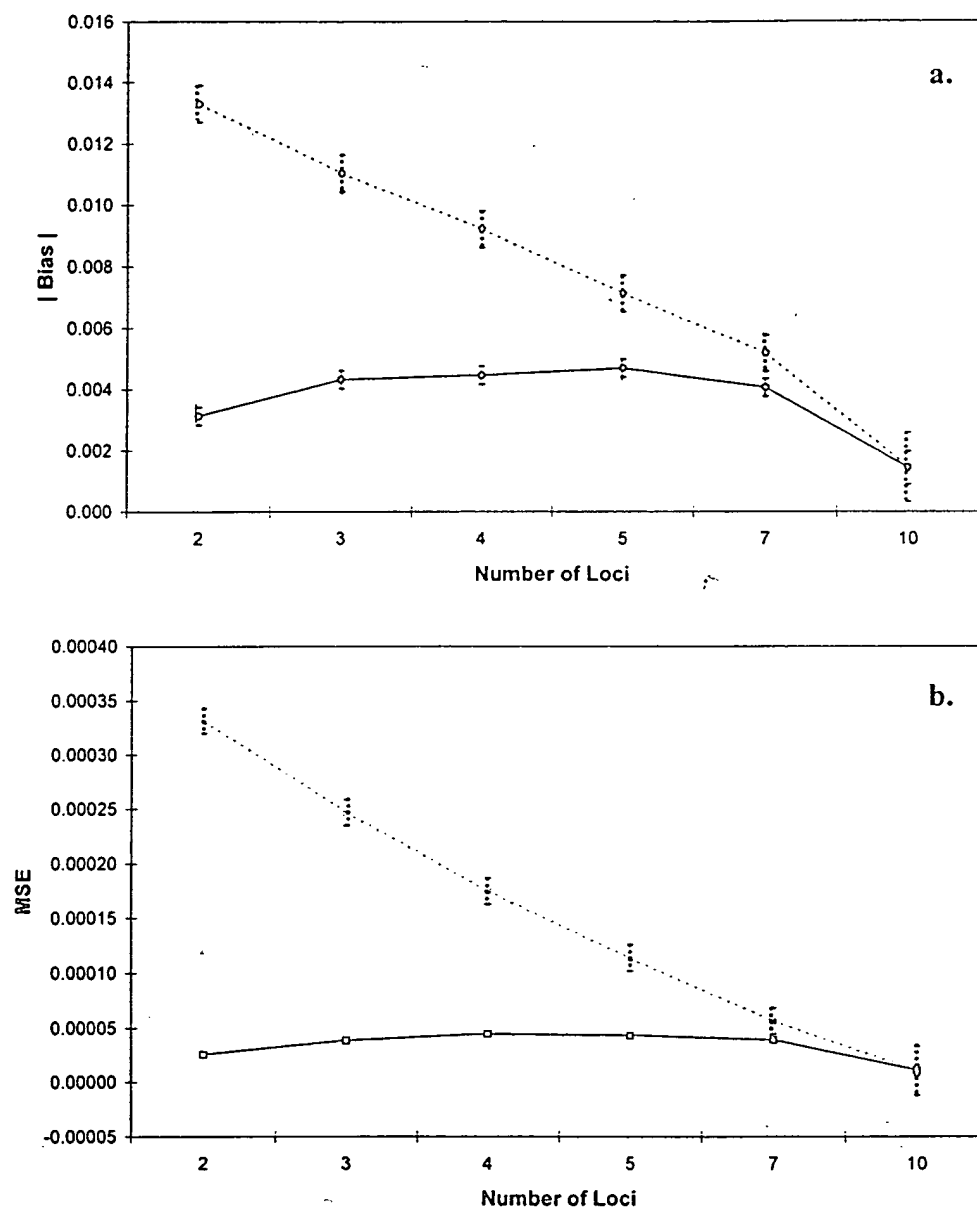


Figure 13

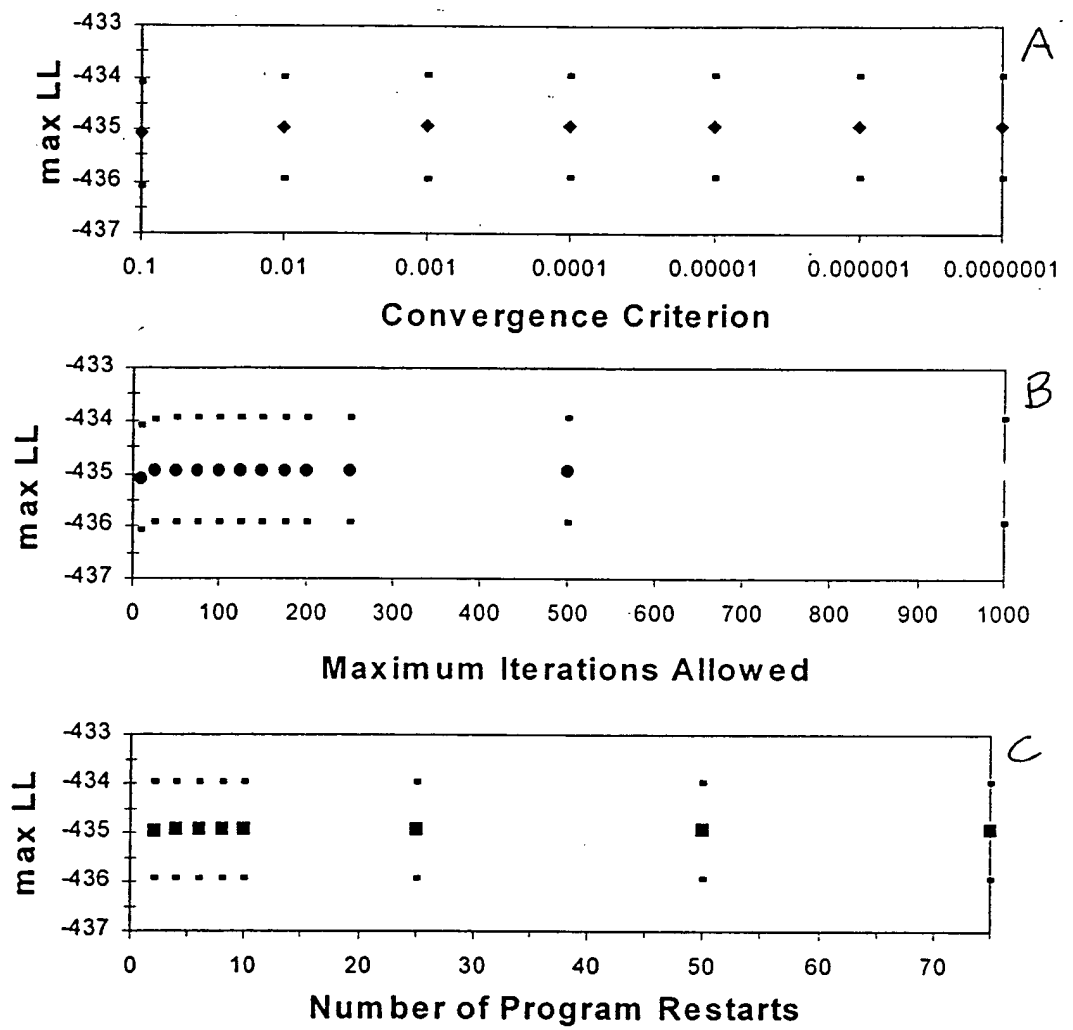


Figure 7

Table. Haplotype Frequency Estimates and Significance Levels of Case-control Comparison from Permutation Tests

Chromosome 19 APOE Gene Region:											
Configuration 1						Configuration 2:					
M1 M2 M3 M4* M5 M6 M7 M8						M1 M2 M3 M4* M5 M6 M7 M8					
* part of $\epsilon 4$ allele determination						* part of $\epsilon 4$ allele determination					
(APOE ϵ SNP included in haplotypes)						(Loci included flank the APOE $\epsilon 4$ SNP)					
Haplotype	Overall	Case	Control	χ^2	P value*	Haplotype	Overall	Case	Control	χ^2	P value*
TCCA	0.007	0.012	0.000	1.83	0.243	TACA	0.207	0.192	0.220	0.42	0.357
CCCA	0.013	0.022	0.000	3.34	0.025	CACA	0.057	0.050	0.069	0.60	0.357
TTCA	0.009	0.009	0.007	0.04	0.884	TGCA	0.015	0.003	0.034	5.53	0.002
CTCA	0.031	0.049	0.000	7.41	0.014	CGCA	0.166	0.190	0.132	2.10	0.044
TCTA	0.224	0.197	0.258	1.81	0.072	TATA	0.021	0.019	0.023	0.06	0.810
CCTA	0.198	0.189	0.219	0.47	0.285	CATA	0.005	0.009	0.004	0.27	0.776
TTTA	0.000	0.000	0.000	0.00	0.116	TGTA	0.000	0.000	0.000	0.00	0.395
CTTA	0.004	0.006	0.002	0.26	0.837	CGTA	0.008	0.009	0.008	0.02	0.896
TCCG	0.002	0.003	0.000	0.44	0.664	TACG	0.232	0.262	0.195	2.21	0.055
CCCG	0.002	0.004	0.000	0.64	0.562	CACG	0.066	0.049	0.092	2.57	0.061
TTCG	0.088	0.115	0.056	3.56	0.023	TGCG	0.013	0.000	0.032	6.67	0.000
CTCG	0.079	0.110	0.042	5.22	0.023	CGCG	0.176	0.189	0.152	0.83	0.209
TCTG	0.138	0.124	0.159	0.85	0.276	TATG	0.000	0.000	0.000	0.00	0.285
CCTG	0.180	0.135	0.228	5.01	0.008	CATG	0.018	0.014	0.022	0.33	0.606
TTTG	0.017	0.014	0.017	0.04	0.78	TGTG	0.000	0.000	0.000	0.00	0.619
CTTG	0.010	0.010	0.012	0.04	0.846	CGTG	0.016	0.015	0.018	0.05	0.804
Likelihoods:	-1117.2	-668.7	-416.9	63.12**	0.0001		-1149.7	-621.6	-511.5	33.34**	0.0041
Other Haplotype Configurations and Significance Levels											
Chromosome 19 region											
Configuration 3:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes contain 4 locus				LRT **		P value*			
Configuration 4:	M1 M2 M3 M4* M5 M6 M7 M8							93.66			
Configuration 5:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes flank 4 locus						57.39			
Configuration 6:	M1 M2 M3 M4* M5 M6 M7 M8	Haplotypes do not contain or flank 4 locus						45.64			
Configuration 7:	M1 M2 M3 M4 M5	Haplotypes in 'control' region						13.48			
Configuration 8:	M1 M2 M3 M4 M5							17.29			
								6.49			

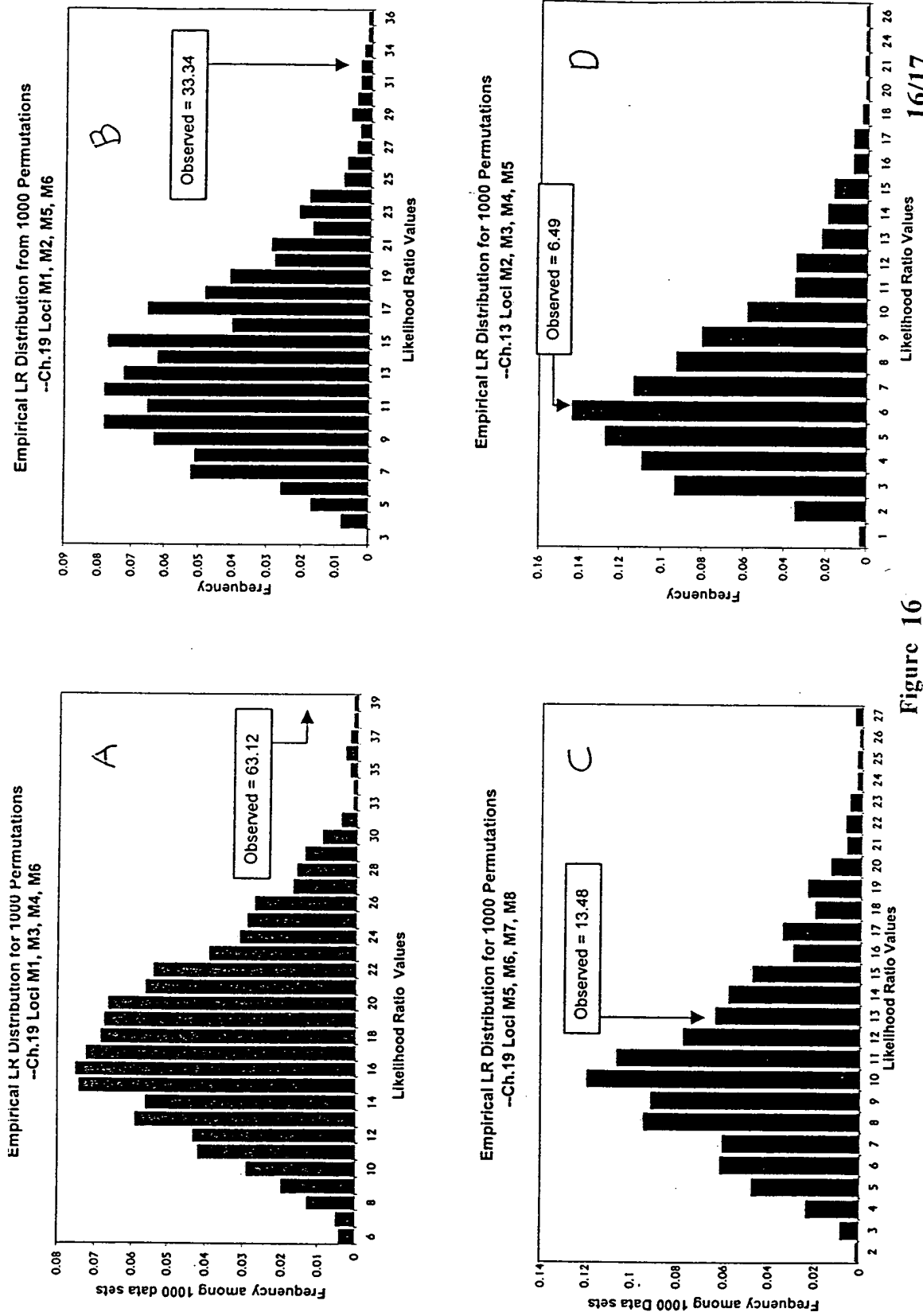


Figure 16